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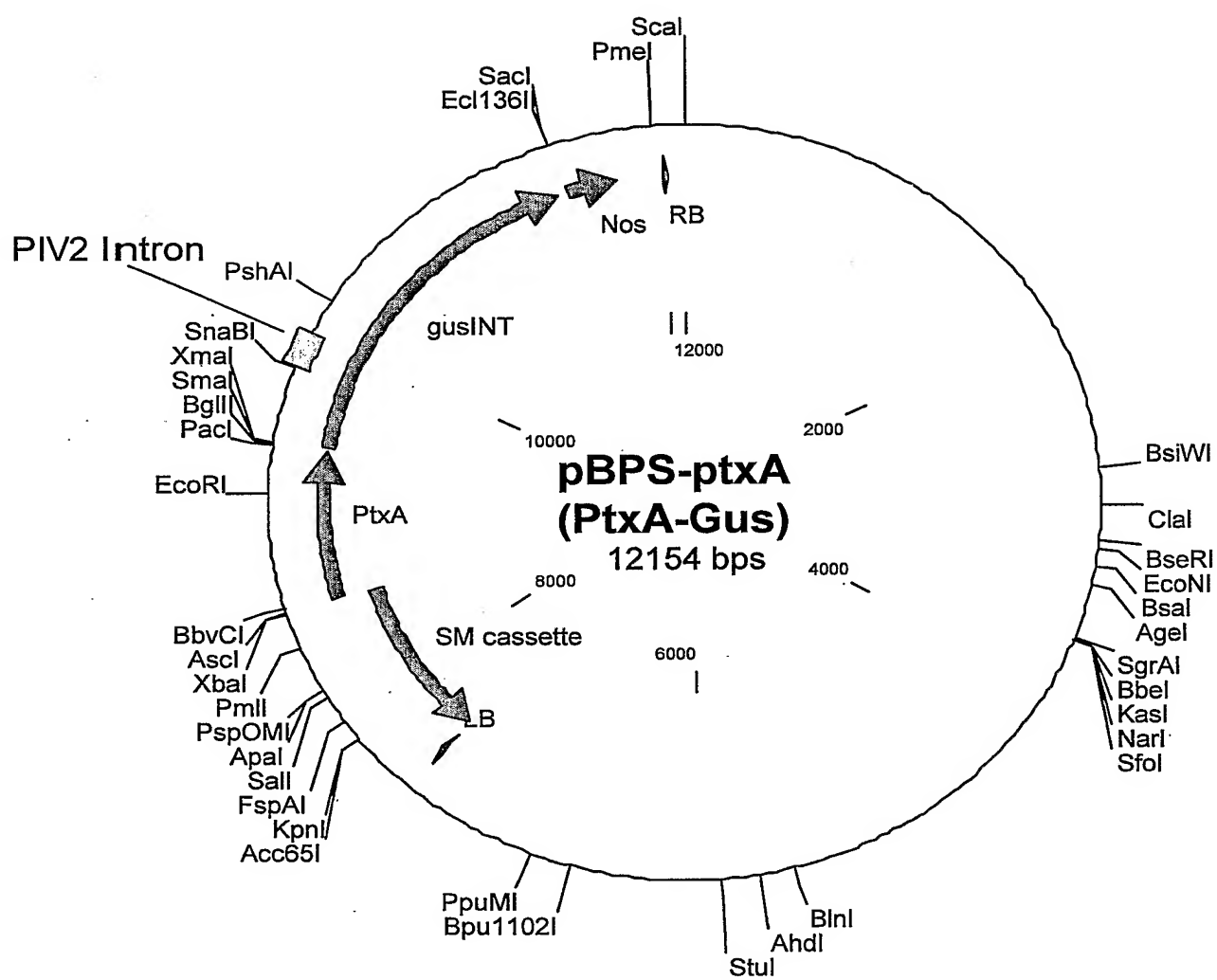


Fig. 1

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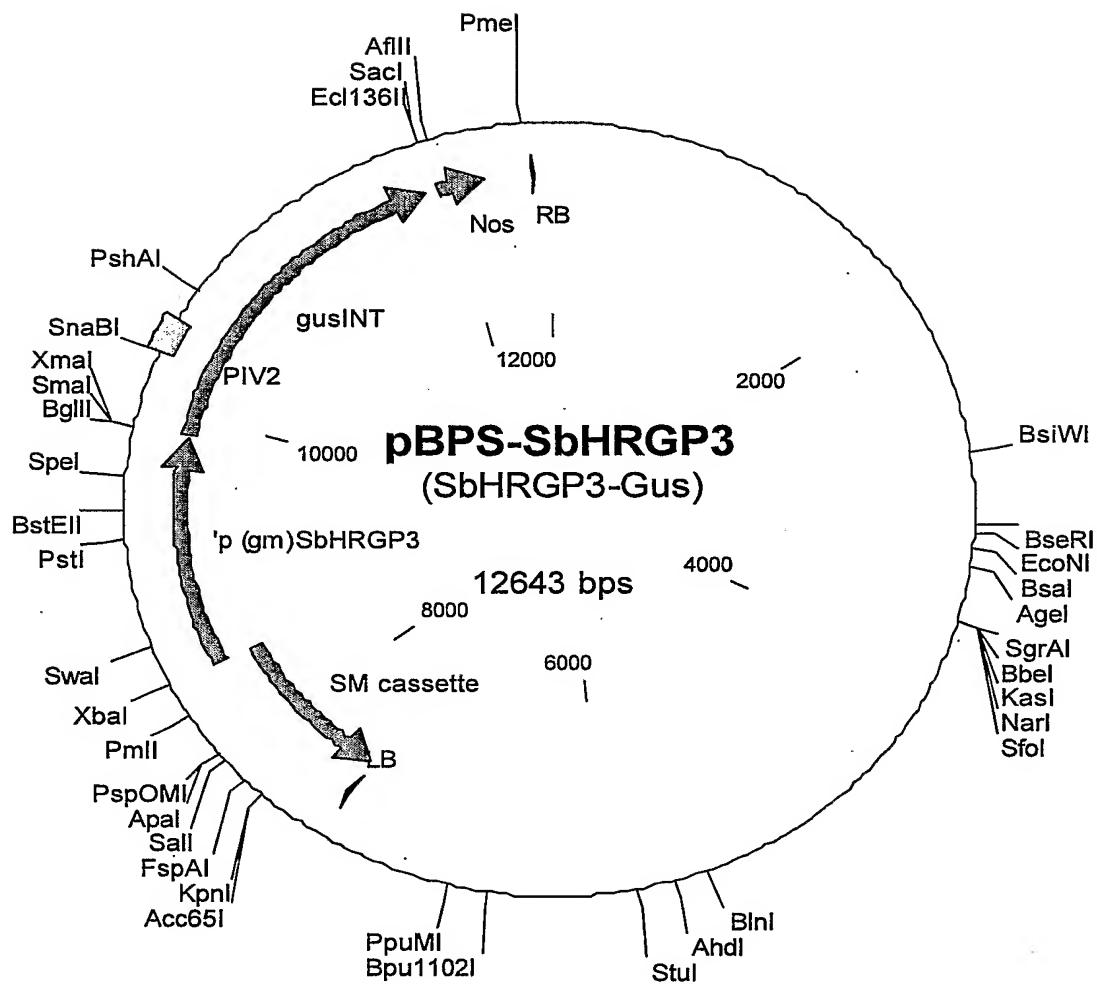
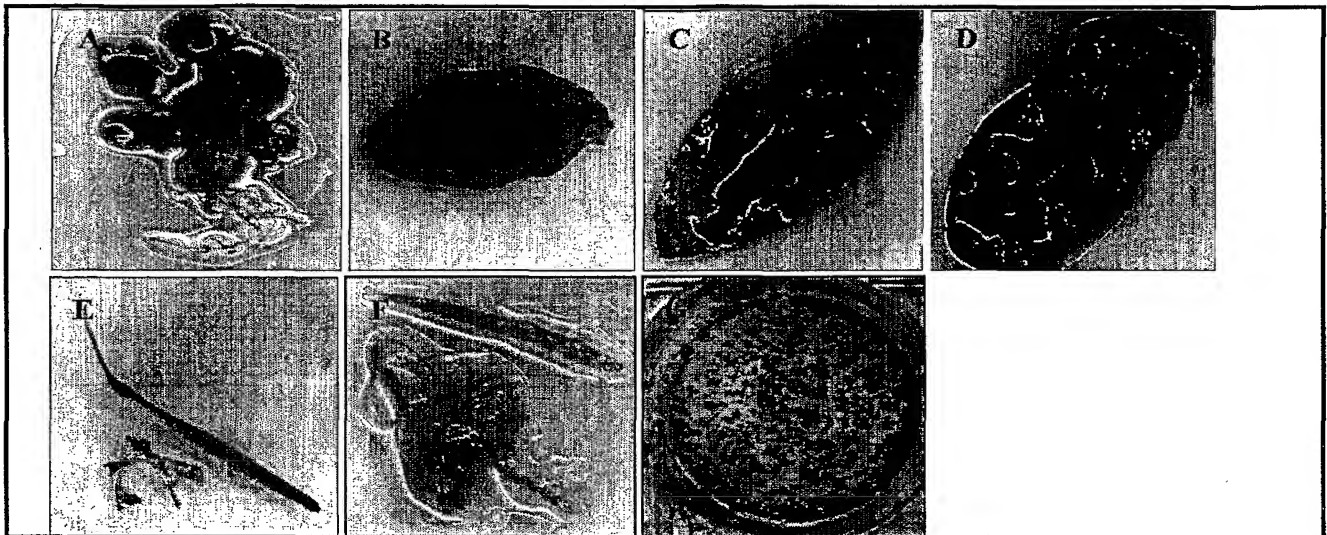


Fig. 2

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I



II

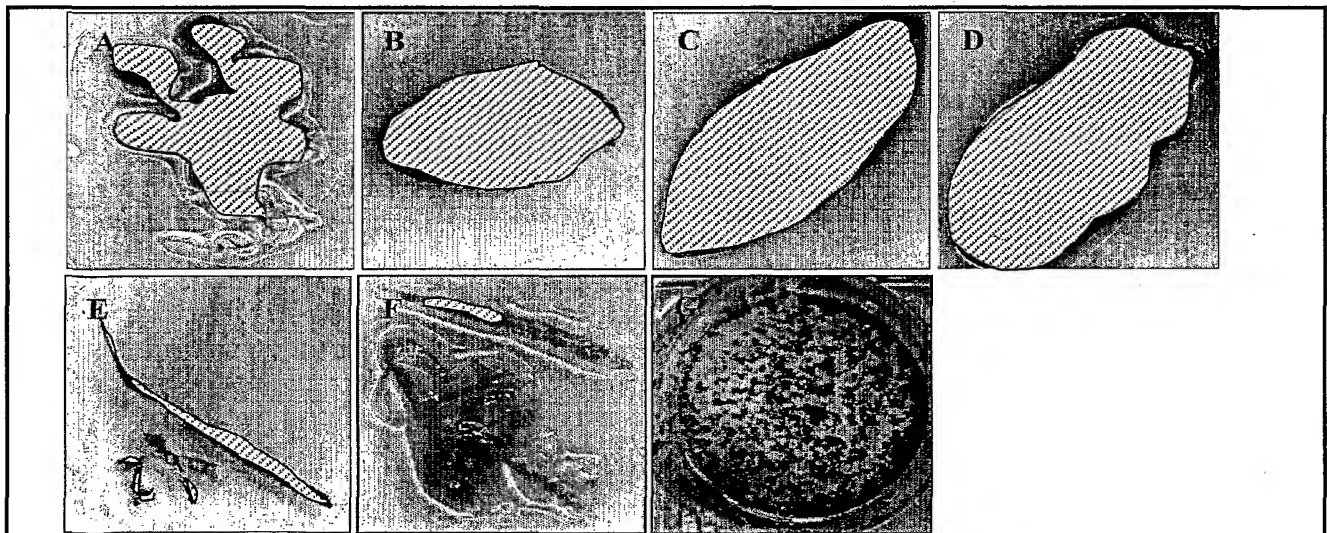
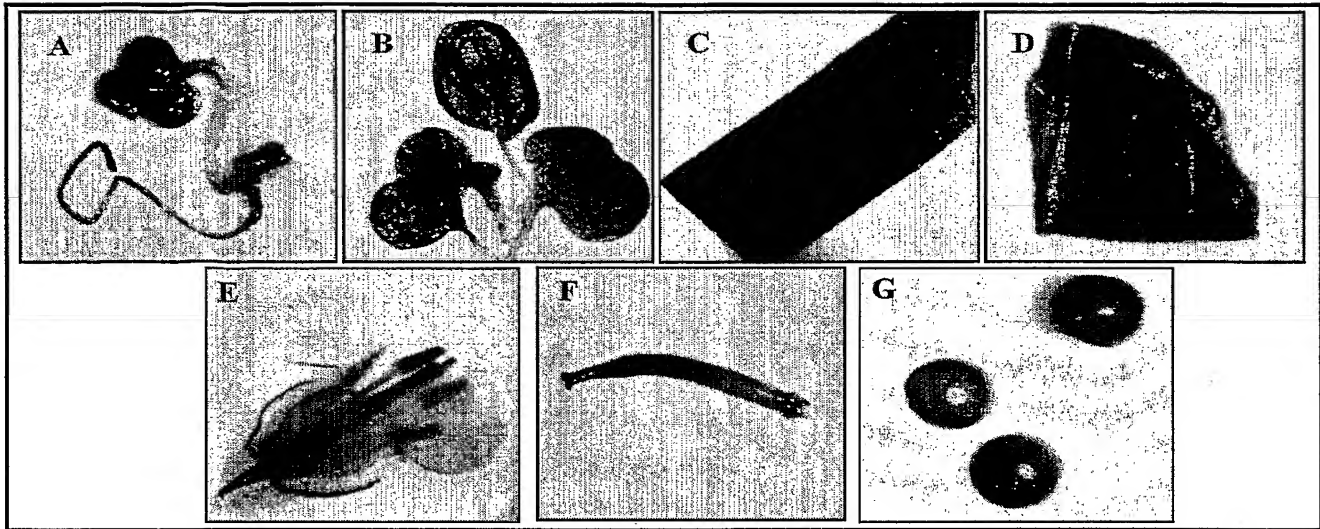


Fig 3

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I



II

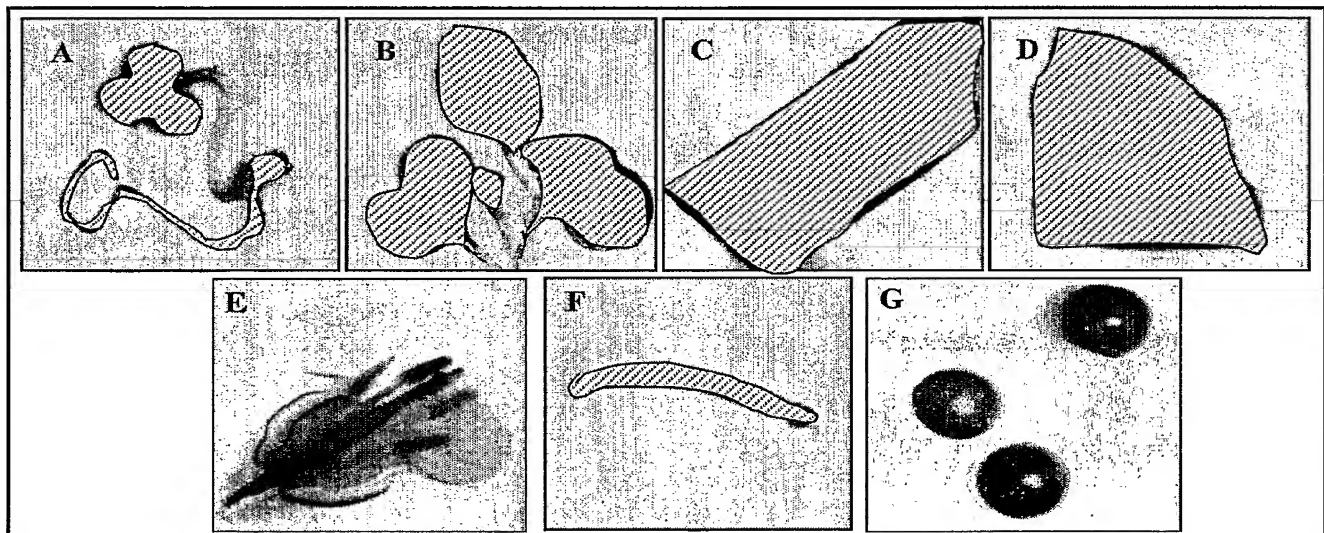


Fig 4

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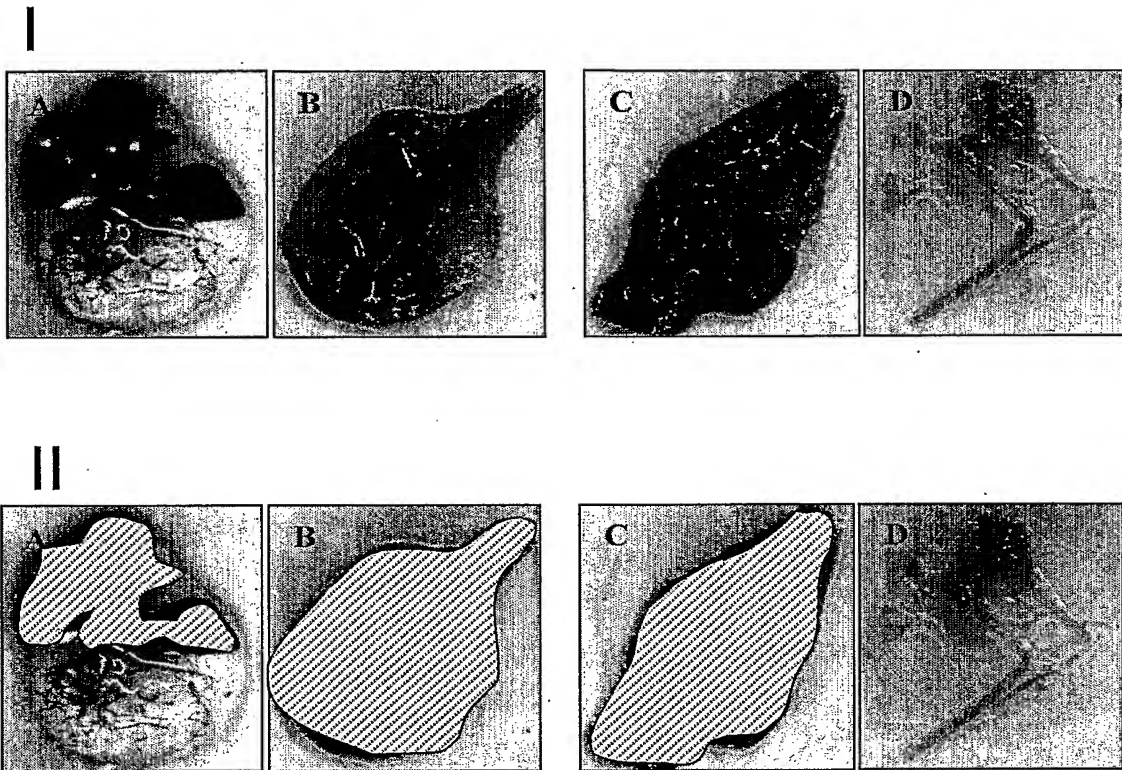


Fig 5

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	1	50
A	(1) MANFAIANVLILLNLSTLLNVLACPYCPYSPKPPTHKPPIVKPPVHK-	
B	(1) MANYALANVFILLNLSTLLIVLACPYCPYSPKPPTHHPPIVKPPVHKR	
C	(1) -----	
D	(1) -PHVKPPSTPKHPKDPHVKPPSTPKQPPYVKPPTTPKHPPHVKPPS---	
E	(1) MGKHGLATWLVILLNFATLLTSLACSYCPSPP-----	
F	(1) MGSRLASEFVFLIFTVITLPTIQACTPCTRPHPPVVKP-----	
Consensus	(1) MA ALAS ILLN STLL LAC YCPYSP PP PP VKPP	
	51	100
A	(50) -----PPKPQPCPPSSSPKPPHVKPPPHYKPPAVHP	
B	(51) RKYSPTPKPPVHKPPRYPPKPSPCPPSSSTPKPPHVKPPHHKPPVVHP	
C	(1) -----RAESART	
D	(47) -----TPKHPPKPP-----QKPCPPSHHGKPPIVKP	
E	(35) -----KPP-----KVKHPLPPLPPKHPPHVKP	
F	(41) -----PQHGGGGGGGSKPPPHGGGKGGGKPP	
Consensus	(51) PK PP K PH PPP H PKPP VKP	
	101	150
A	(83) PHVPKPP-AVHPPHVKPPVHPPIVHPPYVPK-----PPVVKPP-----	
B	(101) PHVPKP--PVHPPYVPKPPIVKPPIVHPPYVPK-----PPVVKPPPYVPK	
C	(8) HHMFQP---HPP-YVPKPPIVKPPIVHPPYVPK-----PPVVKPP-----	
D	(75) PHVPRPP-IVHPPPIVSPSTPKPPKTPFTPKPPSPPIPIVSPP-----	
E	(57) PHTPMP-----PNPPAVKPPYVPK-----PPVVEPP-----	
F	(67) PHGGKGGGPPHHGGGGGGGKSPVVRPPPVVVRP---PPIIRPP-----	
Consensus	(101) PHVPKP VHPYVPKPPIV PPIVHPPYVPK PPVVKPP	
	151	200
A	(122) --VVKPPHVKPPVVPVTPPYIPKPPIVFPPHVPLPP--VVPVTPPYVPK	
B	(144) PPVVRPPYVPKPPVVPVTPPYVPKPPVVRPPYVPKPP--VVPVTPPYVPK	
C	(44) -----PYVPKPPVVRPPYVPKPP--VVPVTPPYVLS	
D	(119) -----IVYPPITPTPIVHPPVTPKPPSPTPIIVSPPIVY	
E	(83) -----YVPKPPVVKPPYVPKPP--PVVEPPYMP	
F	(109) -----PVVYPPPIVRPPPIITRPPIIIPPIQPPPVTT	
Consensus	(151) V PPYVPKPPIVRPPYVPKPP VVPVTPPYVL	
	201	250
A	(168) P-----PIVFPPHVPLPPVVPVTPPYVP-----KPPIVFPPHVPLPPVVP	
B	(192) PPIVKPPIVFPPHVPLPPVVPSPPPYVSPPIVKPPIVFPPHVPLPPVVP	
C	(73) HHCFF-TTVSTSSCTITTTLCTNTPIVN-----HQLFFHHMFFYLPVVP	
D	(154) PPITPTPPVSPPIIPTPIIVSPFFVPN-----PPVV	
E	(108) -----	
F	(140) PPGLLPPIITPPG--LLPPVTTPPGLLP-----PVTTPPG	
Consensus	(201) PP PIV PP V L P V SPPPIVP I F PL PVVP	
	251	300
A	(208) VTPPYVPLPPVVPVTPPPFVPTPPIITPTPTVPVPSPPSETPCPPPPPTV	
B	(242) VTPPYVQPP--PIVTPPTPTPPIVTPPVVSPTP--PSETPCPPPLVP	
C	(116) VTPPYVQPT-----TYCNSTNTNTSNWTPPTP--PSETLVLPPLVP	
D	(186) IPPPYVPSPP-----PVVTPPIVTPPTPCPP-----PPPPPAI	
E	(108) -----H	
F	(173) LLPPIINPP-----PVTVPPPSGGYPPYG-----PPSGG	
Consensus	(251) VTPPYVQPP P IV PP TPPTP PSET PPPP	

Fig. 6a

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	301	350
A	(258)	VPYPPPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCGPLLQGLVD
B	(287)	YPPTPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCGPLLQGLVD
C	(156)	YP-PPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCGPLLQGLVD
D	(219)	IP-SPPAQPTCPIDALKLGACVDVLGGLIHIGIGGSAKQTCGPLLQGLVD
E	(109)	DT-----L---KLGACVDLLGGLVHIGIGSSAKDTCCPVLQGLVD
F	(202)	GGGGGGKQPTCPINALKLGACVDVLGGLIHIGLGNPVENVCCPVLQGLLE
Consensus	(301)	P PPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCGPLLQGLVD

	351	397
A	(308)	LDAAVCLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPSS-
B	(337)	LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAY-
C	(205)	LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAS-
D	(268)	LDAAICLCTTIRLKLLNINIILPIALQVLIDDCGKYPPKDFKCPST-
E	(146)	LDAAVCLCTAIKVKLLNVNIIPIALQVLVG-CGKTTPPSGFQCPA--
F	(252)	LEAAVCLCTTIRLKLLNLNIFIPLALQALIT-CGINPPSGFVCPPLT
Consensus	(351)	LDAAICLCTTIRLKLLNINIVIPALQVLID CGKTPPEGFKCPAS

Fig. 6b

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551                                     600
B      (551) AAAAAC TAAAAAATAATTTCTCTCCTGATTTATATGAAATGACATTTTTTT
A      (1)  -----CGCAATTTTTTT
Consensus (551)                                     G ATTTTTTT
601                                     650
B      (601) TGGAACATGAAGG-GTATTGATTTTTTACCACCTTTTACACCT--TTCAAA
A      (12) GTGAAGCTGAGGGAGGATTGGATTTTACACCTATTCAAAAGTCATTCAAA
Consensus (601) GAA TGA GG G ATTG TTTTAC C TT A A T TTCAAA
651                                     700
B      (648) G-----CCATTCAAGGATGAATATAGATTTTTTGGGCGATCAAACAC
A      (62) GTTGTCCCTCCATTCAAGGATGAATGTAGATTTTTTCAAGCATCAAACAC
Consensus (651) G CCATTCAAGGATGAAT TAGATTTTTT ATCAAACAC
701                                     750
B      (689) AAGAATCATTACGATAACATGCTTTGGAACACACACATGCTTAAATTAAT
A      (112) AAGAATCACTAGCATAACATGCTTTGAAACCCACACA--CTTAAATTAAT
Consensus (701) AAGAATCA TA ATAACATGCTTTG AAC CACACA CTTAAATTAAT
751                                     800
B      (739) GGTGGAGTATCAAAT----TTTAAAT-ATTGTTGTCAAT-ACATACCC
A      (160) GTTAGGAATATCAAATCCAATATAAAATCATAGTTGTCAATTACATACTC
Consensus (751) G T GGA TATCAAAT T TAAAT AT GTTGTCAAT ACATAC C
801                                     850
B      (783) CGTCAATCTTCTTTTTTTTACCCAATAAACATTGAAATGTTGCTTCTTTC
A      (210) AATCAAGTCCCTTTCTTTTACCCAATAAACATCAACATATGTGCTTCTTCC
Consensus (801) TCAA CTTT TTTTACCCAATAAACAT A AT TTGCTTCTT C
851                                     900
B      (833) GTTAAGCATAAAAAACATCAAAGTCTA-----GCAAAATGTTGTTTTTGC
A      (260) ATTAAGCATATAAACATCAAAGTCTAAACTAGCAAAATGTTGTTTTTAG
Consensus (851) TTAAGCATA AAACATCAAAGTCTA GCAAAATGTTGTTTTT
901                                     950
B      (877) GATGACACATTTTCATA--TAGTTTAAAGGATGCATGATTGATTACAAAA
A      (310) GATGACACATTTTCATACATAGTTTAAAGATACTTGATTGATTACAAAA
Consensus (901) GATGACACATTTTCATA TAGTTTAAA GAT C TGATTGATTACAAAA
951                                     1000
B      (925) AAAAAATACTAATAATTCTAGCACAAAGTTTAAAGCAAGATTATAAAGCT
A      (360) AGAAATTACCAATAGTT-TAGCACAAAGTCTAAAGCATAATTA--AAGCA
Consensus (951) A AAA TAC AATA TT TAGCACAAAGT TAAAGCA ATTA AAGC
1001                                     1050
B      (975) TCATAGCATGTGGATATTCATTTAGAAATATAGATTA-GATTGCCCTTT
A      (407) TCA---CATGTGCAGATTTAT---GAAAAAAGATTAAGATTGCCCTTT
Consensus (1001) TCA CATGTG A ATT AT GAAA A AGATTA GATTGCCCTTT
1051                                     1100
B      (1024) CATCACGGGTC---TAACAGCACCCTTGTCACCTACATGTCAAAAA--TG
A      (451) CATCACGGGTCGAATAATAGCACTACTTGTCACCTACATGTAAAAAATG
Consensus (1051) CATCACGGGTC TAA AGCAC ACTTGTCACCTACATGT AAAAA TG
1101                                     1150
B      (1069) TCCTCTAGTACAGCACCGCTTTTTTACTTGATTCCCCTTGTCATGCATGA
A      (501) TCCTCTAGTACATCAAACCTTTTTCCATTGATTCCCCTTATCC----ATGA
Consensus (1101) TCCTCTAGTACA CA TTTT TTGATTCCCCTT TCC ATGA
1151                                     1200
B      (1119) AAAAAATCAAAACAATATTTGGACACACAAACTTGCCCCACCTTTCTTT
A      (547) AAAAAATAAACAATTCCTTAAGACACAAAAAATGGCCCCACAT-CCTTT
Consensus (1151) AAAAAAT AA A A T TT GACACA AAA TG CCCAC T CCTTT

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Fig. 7a

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	1201		1250
B	(1169)	TTCTTTCTGCCCTAGTTTGTGTTGAGACTCATATTGATCAAATTTGGCTAT	
A	(596)	---TTTCTGGCCTAGTTTGTGTTGA-----	
Consensus	(1201)	TTTCTG CCTAGTTTGTGTTGA	
	1251		1300
B	(1219)	GAATTCAAACAAAAAATTCACCTCTACCCATTGCATGTGT---GGGGCCCA	
A	(617)	-----A-----TTCATTCTAACTCTTGAATATGTAACGAGGCCCA	
Consensus	(1251)	A TTCA TCTA C TTG AT TGT G GGCCCA	
	1301		1350
B	(1266)	CATATAAATCCATGAAGGATTTCAATGTCCATCCAAGTCAATGATTCAAC	
A	(652)	C-TAAAAATCAAT-----CAATGATTTAAC	
Consensus	(1301)	C TA AAATC AT CAATGATT AAC	
	1351		1400
B	(1316)	ATATATAACATTGAATAATTTAATTCCAATTTGCAGTATTATGATTTAGA	
A	(676)	ATAAAAAA---TGAATAGTTTAATTCCAATTTGC-----	
Consensus	(1351)	ATA A AA TGAATA TTTAATTCCAATTTGC	
	1401		1450
B	(1366)	TTGATTGCTGCAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGT	
A	(707)	-----TGCAACATGGTCCGTGAATATGA---CTCACGAGAAAGATAT	
Consensus	(1401)	TGCAA A GGTCCGTGAAT TGA CTCACGAGAAAGA T	
	1451		1500
B	(1416)	ATCAAAATTTCAAGGTATTTTATTTATTTTAAACAAATAAAATTTCAAGG	
A	(746)	ATCAAAATATCAA-----AATTTTCATAG	
Consensus	(1451)	ATCAAAAT TCAA AATTTCA G	
	1501		1550
B	(1466)	TCTTGTTACCCATATAAACCTCCTCACTCACACCCAATTCTCTTAAGTGT	
A	(769)	TTTTTTTTCACCATATAAACCTCATCACTCATTC--TATTTTTTTTAAGTGC	
Consensus	(1501)	T TT TTCACCATATAAACCTC TCACTCA C ATT T TTAAGTG	
	1551		1600
B	(1516)	ATGACTTCATAGTAC--ACTACACTACTTTCTTTGAAACATGGCTAACTA	
A	(817)	AAAGCTTCATAGTAGTGAGCACACACATTACACTAAAATCTTCGAAACTT	
Consensus	(1551)	A CTTCATAGTA A ACAC TT C T AAA T AACT	
	1601		1650
B	(1564)	TGCTCTAGCCAATGTTTTTCATCCTTCTCTTGAACCTTGAGTACCTTACTCA	
A	(867)	A-----	
Consensus	(1601)		

Fig. 7b

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	1		50
SEQ ID NO: 9	(1)	---CTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT	
SEQ ID NO: 8	(1)	AAGCTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT	
SEQ ID NO: 7	(1)	AAGCTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT	
Consensus	(1)	AAGCTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT	
	51		100
SEQ ID NO: 9	(48)	CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA	
SEQ ID NO: 8	(51)	CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA	
SEQ ID NO: 7	(51)	CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA	
Consensus	(51)	CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA	
	101		150
SEQ ID NO: 9	(98)	TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA	
SEQ ID NO: 8	(101)	TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA	
SEQ ID NO: 7	(101)	TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA	
Consensus	(101)	TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA	
	151		200
SEQ ID NO: 9	(148)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT	
SEQ ID NO: 8	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT	
SEQ ID NO: 7	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT	
Consensus	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT	
	201		250
SEQ ID NO: 9	(198)	TTCAGTTAAGATTTAAATAGTATAAATTA AAAATTATCGATGATGACAAA	
SEQ ID NO: 8	(201)	TTCAGTTAAGATTTAAATAGTATAAATTA AAAATTATCGATGATGACAAA	
SEQ ID NO: 7	(201)	TTCAGTTAAGATTTAAATAGTATAA- TTA AAAATTATCGATGATGACAAA	
Consensus	(201)	TTCAGTTAAGATTTAAATAGTATAAATTA AAAATTATCGATGATGACAAA	
	251		300
SEQ ID NO: 9	(248)	AAATTGTAAATATAATTCATTTTAAAAAAGTTAAGAAATTGAAAAAGGA	
SEQ ID NO: 8	(251)	AAATTGTAAATATAATTCATTTTAAAAAAGTTAAGAAATTGAAAAAGGA	
SEQ ID NO: 7	(250)	AAATTGTAAATATAATTCATTTTAAAAAAGTTAAGAAATTGAAAAAGGA	
Consensus	(251)	AAATTGTAAATATAATTCATTTTAAAAAAGTTAAGAAATTGAAAAAGGA	
	301		350
SEQ ID NO: 9	(298)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA	
SEQ ID NO: 8	(301)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA	
SEQ ID NO: 7	(300)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA	
Consensus	(301)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA	
	351		400
SEQ ID NO: 9	(348)	TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA	
SEQ ID NO: 8	(351)	TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA	
SEQ ID NO: 7	(350)	TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA	
Consensus	(351)	TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA	
	401		450
SEQ ID NO: 9	(398)	ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG	
SEQ ID NO: 8	(401)	ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG	
SEQ ID NO: 7	(400)	ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG	
Consensus	(401)	ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG	
	451		500
SEQ ID NO: 9	(448)	TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG	
SEQ ID NO: 8	(451)	TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG	
SEQ ID NO: 7	(450)	TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG	
Consensus	(451)	TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG	
	501		550

Fig. 8a

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SEQ ID NO: 9(498) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
SEQ ID NO: 8(501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
SEQ ID NO: 7(500) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
Consensus      (501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
                    551                                     600

SEQ ID NO: 9(548) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 8(551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 7(550) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
Consensus      (551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
                    601                                     650

SEQ ID NO: 9(598) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 8(601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 7(600) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
Consensus      (601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
                    651                                     700

SEQ ID NO: 9(648) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAGCAAAA-----
SEQ ID NO: 8(651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAGCAAAA-----
SEQ ID NO: 7(650) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAGCAAAAAGCAAAA
Consensus      (651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAGCAAAA
                    701                                     750

SEQ ID NO: 9(692) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 8(695) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 7(700) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
Consensus      (701) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
                    751                                     800

SEQ ID NO: 9(742) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 8(745) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 7(750) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
Consensus      (751) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
                    801                                     850

SEQ ID NO: 9(792) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 8(795) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 7(800) TGCAATATGCACATATTCGTTTTAGGCTTTTAGC-TCCACGATCTGTTAA
Consensus      (801) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
                    851                                     900

SEQ ID NO: 9(842) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 8(845) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 7(849) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
Consensus      (851) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
                    901                                     950

SEQ ID NO: 9(892) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
SEQ ID NO: 8(895) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
SEQ ID NO: 7(899) CAGGGAAGCACTAGAAGATATGAAATGAC-TAAAAGGTCACCATGCATAA
Consensus      (901) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
                    951                                     1000

SEQ ID NO: 9(942) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 8(945) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 7(948) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
Consensus      (951) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT

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Fig. 8b

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1001                                     1050
SEQ ID NO: 9(992) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 8(995) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 7(998) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
Consensus (1001) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
1051                                     1100
SEQ ID NO: 9(1042) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 8(1045) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 7(1048) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
Consensus (1051) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
1101                                     1150
SEQ ID NO: 9(1092) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 8(1095) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 7(1098) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
Consensus (1101) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
1151                                     1200
SEQ ID NO: 9(1142) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
SEQ ID NO: 8(1145) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
SEQ ID NO: 7(1148) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
Consensus (1151) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
1201                                     1250
SEQ ID NO: 9(1192) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 8(1195) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 7(1198) CCAACTTGGT-----CCAAAAAACTCAATATCAATATTTTCGAAAT
Consensus (1201) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
1251                                     1300
SEQ ID NO: 9(1242) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 8(1245) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 7(1239) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
Consensus (1251) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
1301                                     1350
SEQ ID NO: 9(1292) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 8(1295) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 7(1289) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAA-GTTGTAT
Consensus (1301) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
1351                                     1393
SEQ ID NO: 9(1342) AAAGGGCAACACTACCTCTCCTAATGGCAGTA-----
SEQ ID NO: 8(1345) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
SEQ ID NO: 7(1338) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
Consensus (1351) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG

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Fig. 8c

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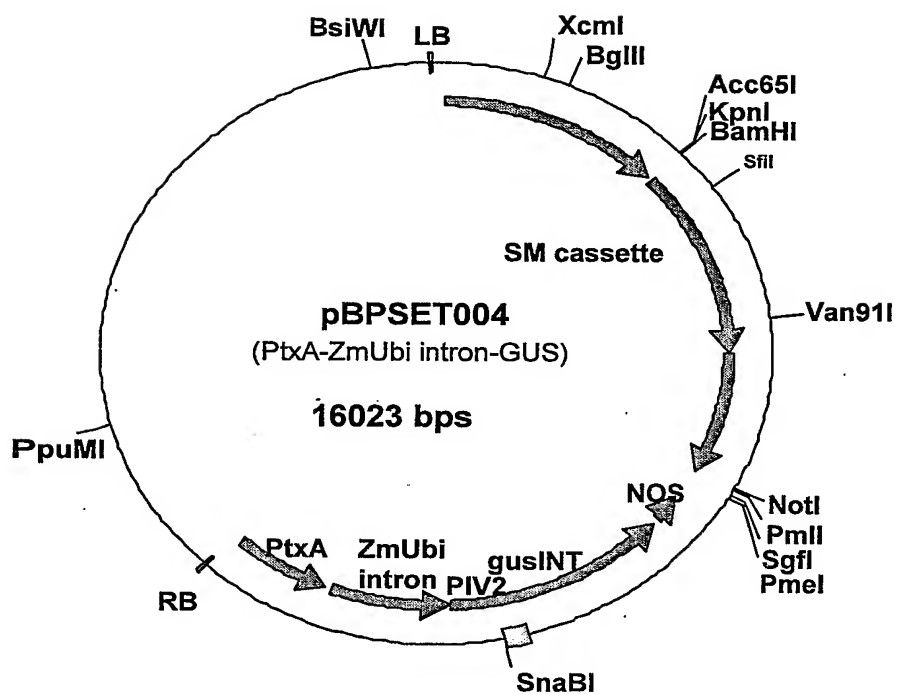


Fig. 9